Claims

1. A method for identifying individuals susceptible to osteoarthritis comprising obtaining a sample of genomic DNA and detecting the presence or absence of the 258bp allele of D11S937 from chromosome 11.

2. A method according to claim 1 for identifying individuals susceptible to osteoarthritis of the hip.

3. A method according to any one of claims 1 and 2 for identifying female individuals susceptible to osteoarthritis.

4. A method for isolating genetic loci associated with susceptibility to OA comprising screening a genomic library from an individual who is homozygote for the 258 bp allele of D11S937 and identifying open reading frames in regions adjacent to said allele.

5. A method for isolating genetic loci associated with susceptibility to OA comprising identifying open reading frames in regions adjacent to D11S937 and comparing said open reading frames in individuals carrying a 258 bp allele of D11S937 with said open reading frames in individuals with a non-258 bp allele of D11S937.

6. A method for isolating genetic loci according to any one of claims 4 and 5 in which open reading frames are identified within 500 Kb of D11S937.

7. The use of the 258bp allele of D11S937 as a marker for the identification of loci influencing susceptibility to OA.

8. The use of the 258 bp allele of D11S937 according to claim 7 wherein the loci contain an ancestral DNA variant conferring enhanced OA susceptibility.

9. The use of the 258 bp allele of D11S937 according to claim 7 to identify genes associated with OA susceptibility.

10. A method for identifying sequences which affect susceptibility to OA by comparing genomic regions containing the 258 bp allele of D11S937 with genomic regions containing other alleles of D11S937.

11. A method for determining individual susceptibility to osteoarthritis comprising obtaining sample genomic DNA from siblings, at least two of which have clinical symptoms of osteoarthritis, analysing a region of their genomic DNA comprising any one of the polymorphic markers; D2S202, D3S1266, D4S231, D4S415, D6S260, D6S273, D6S286, D6S281, D7S669, D7S530, D11S907, D11S903, D11S901, D17S807, D17S789, DXS1068, identifying allele sharing between the siblings as defined by a maximum log of the odds (LOD) score of greater than 1 and a p-value of less then 0.25, and determining individual susceptibility to osteoarthritis by reference to the allele sharing.

12. A method for determining individual susceptibility to osteoarthritis according to claim 10 in which a region of genomic DNA is analysed which comprises one or more of the following polymorphic markers; D11S901, D11S903, D11S907.

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13. A method for determining individual susceptibility to osteoarthritis according to claims 10 and 11 in which the analysed region of genomic DNA comprises a polymorphic marker located within 20cM of DS11901.

14. A method for determining individual susceptibility to osteoarthritis according to claim 10 in which a region of genomic DNA is analysed which comprises one or more of the following polymorphic markers; D6S273, DXS1068.

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15. A method for determining individual susceptibility to

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osteoarthritis according to any one of claims 10 to 12 in which one or more of the following genomic regions is additionally analysed; a genomic region comprising the polymorphic marker D6S273 and a genomic region comprising the polymorphic marker DXS1068.

16. A method for identifying loci conferring susceptibility to osteoarthritis comprising screening a genomic library with genetic sequence derived from one or more of the following polymorphic markers; D2S202, D3S1266, D4S231, D4S415, D6S260, D6S273, D6S286, D6S281, D7S669, D7S530, D11S907, D11S903, D11S901, D17S807, D17S789, DXS1068 and identifying open reading frames in regions adjacent to the marker.

17. A method according to claim 15 in which the open reading frames identified are located within 500 Kb of the polymorphic marker.

18. A method for isolating genetic loci associated with susceptibility to OA comprising screening a genomic library with sequence derived from the region between polymorphic markers D11S1358 and D11S35 and identifying open reading frames in regions adjacent to the markers.